

CRF Correctors Corrected by the STIC Systems Branch  
Serial Number: 09/672,725B

CRF Processing Date: 10/22/2002  
Edited by: \_\_\_\_\_  
Verified by: \_\_\_\_\_ (STIC staff)

1600

- Changed a file from non-ASCII to ASCII
- Changed the margins in cases where the sequence text was "wrapped" down to the next line. 1659
- Edited a format error in the Current Application Data section, specifically:
- Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_
- Added the mandatory heading and subheadings for "Current Application Data".
- Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
- Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
- Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- Inserted colons after headings/subheadings. Headings edited included:
- Deleted extra, invalid, headings used by an applicant, specifically:
- Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  
 page numbers throughout text;  other invalid text, such as \_\_\_\_\_
- Inserted mandatory headings, specifically: **RECEIVED**
- Corrected an obvious error in the response, specifically: **OCT 25 2002**
- Edited identifiers where upper case is used but lower case is required, or vice versa. **TECH CENTER 1600/2900**
- Corrected an error in the Number of Sequences field, specifically:
- A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- Other: \_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/672,725B**

DATE: 10/22/2002  
TIME: 19:21:18

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\10222002\I672725B.raw

4 <110> APPLICANT: Stocker, Penny J.  
5 Steimel-Crespi, Dorothy T.  
6 Crespi, Charles L.  
7 Rief, Timothy C  
8 Patten, Christopher J.  
10 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
13 <130> FILE REFERENCE: G0307/7017  
15 <140> CURRENT APPLICATION NUMBER: US 09/672,725B  
16 <141> CURRENT FILING DATE: 2000-09-28  
18 <150> PRIOR APPLICATION NUMBER: US 60/156,510  
19 <151> PRIOR FILING DATE: 1999-09-28  
21 <160> NUMBER OF SEQ ID NOS: 32  
23 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 4279  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Canis familiaris  
30 <220> FEATURE:  
31 <221> NAME/KEY: CDS  
32 <222> LOCATION: (17)...(3859)  
34 <400> SEQUENCE: 1

RECEIVED

OCT 25 2002

TECH CENTER 1600/2900

35	ggagcgcgag	gtcggg	atg	gat	cct	gaa	gga	ggc	cgt	aag	ggg	agt	gca	gag	52		
36			Met	Asp	Pro	Glu	Gly	Gly	Arg	Lys	Gly	Ser	Ala	Glu			
37			1				5						10				
39	aag	aac	ttc	tgg	aaa	atg	ggc	aaa	aaa	agt	aaa	aaa	aat	gag	aaa	100	
40	Lys	Asn	Phe	Trp	Lys	Met	Gly	Lys	Lys	Ser	Lys	Lys	Asn	Glu	Lys	Lys	
41													15	20	25		
43	gaa	aag	aaa	cca	act	gtc	agc	acg	ttt	gca	atg	ttt	cgc	tat	tca	aat	148
44	Glu	Lys	Lys	Pro	Thr	Val	Ser	Thr	Phe	Ala	Met	Phe	Arg	Tyr	Ser	Asn	
45													30	35	40		
47	tgg	ctt	gat	agg	ttg	tat	atg	ttg	gtg	ggg	aca	atg	gct	gcc	atc	atc	196
48	Trp	Leu	Asp	Arg	Leu	Tyr	Met	Leu	Val	Gly	Thr	Met	Ala	Ala	Ile	Ile	
49													45	50	55	60	
51	cat	gga	gct	gca	ctc	cct	ctc	atg	atg	ctg	gtt	ttt	gga	aac	atg	aca	244
52	His	Gly	Ala	Ala	Leu	Pro	Leu	Met	Met	Leu	Val	Phe	Gly	Asn	Met	Thr	
53													65	70	75		
55	gat	agc	ttt	gca	aat	gca	gga	att	tca	aga	aac	aaa	act	ttt	cca	gtt	292
56	Asp	Ser	Phe	Ala	Asn	Ala	Gly	Ile	Ser	Arg	Asn	Lys	Thr	Phe	Pro	Val	
57													80	85	90		
59	ata	att	aat	gaa	agt	att	acg	aac	aat	aca	caa	cat	ttc	atc	aac	cat	340
60	Ile	Ile	Asn	Glu	Ser	Ile	Thr	Asn	Asn	Thr	Gln	His	Phe	Ile	Asn	His	
61													95	100	105		
63	ctg	gag	gag	gaa	atg	acc	acg	tat	gcc	tat	tat	tac	agt	ggg	atc	ggt	388

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64	Leu	Glu	Glu	Glu	Met	Thr	Thr	Tyr	Ala	Tyr	Tyr	Ser	Gly	Ile	Gly		
65	110					115						120					
67	gct	ggc	gtg	ctg	gtg	gct	tac	atc	cag	gtt	tca	ttc	tgg	tgc	ctg	436	
68	Ala	Gly	Val	Leu	Val	Ala	Ala	Tyr	Ile	Gln	Val	Ser	Phe	Trp	Cys	Leu	
69	125					130					135				140		
71	gca	gca	gga	aga	cag	ata	ctc	aaa	att	aga	aaa	caa	ttt	ttt	cat	gct	484
72	Ala	Ala	Gly	Arg	Gln	Ile	Leu	Lys	Ile	Arg	Lys	Gln	Phe	Phe	His	Ala	
73						145					150				155		
75	atc	atg	cga	cag	gag	att	ggc	tgg	ttt	gac	gtg	cat	gac	gtt	ggg	gag	532
76	Ile	Met	Arg	Gln	Glu	Ile	Gly	Trp	Phe	Asp	Val	His	Asp	Val	Gly	Glu	
77						160				165				170			
79	ctt	aac	acc	cgg	ctc	aca	gac	gat	gtc	tcc	aaa	atc	aat	gaa	gga	att	580
80	Leu	Asn	Thr	Arg	Leu	Thr	Asp	Asp	Val	Ser	Lys	Ile	Asn	Glu	Gly	Ile	
81						175				180			185				
83	ggc	gac	aaa	att	gga	atg	ttc	ttt	cac	tca	ata	gca	aca	ttt	ttc	acc	628
84	Gly	Asp	Lys	Ile	Gly	Met	Phe	Phe	His	Ser	Ile	Ala	Thr	Phe	Phe	Thr	
85						190			195			200					
87	ggt	ttt	ata	gtg	ggg	ttt	aca	cgt	ggt	tgg	aag	cta	acc	ctt	gtg	att	676
88	Gly	Phe	Ile	Val	Gly	Phe	Thr	Arg	Gly	Trp	Lys	Leu	Thr	Leu	Val	Ile	
89						205			210			215			220		
91	ttg	gcc	atc	agc	cct	gtt	ctt	gga	ctt	tca	gcc	atc	tgg	gca	aag		724
92	Leu	Ala	Ile	Ser	Pro	Val	Leu	Gly	Leu	Ser	Ala	Ala	Ile	Trp	Ala	Lys	
93						225			230			235					
95	ata	cta	tct	tca	ttt	act	gat	aaa	gaa	ctc	ttg	gcc	tat	gca	aaa	gct	772
96	Ile	Leu	Ser	Ser	Phe	Thr	Asp	Lys	Glu	Leu	Leu	Ala	Tyr	Ala	Lys	Ala	
97						240			245			250					
99	gga	gca	gta	gct	gaa	gaa	gtc	tta	gca	gca	atc	aga	act	gtg	att	gcc	820
100	Gly	Ala	Val	Ala	Glu	Glu	Val	Leu	Ala	Ala	Ile	Arg	Thr	Val	Ile	Ala	
101						255			260			265					
103	ttt	gga	gga	caa	aag	aaa	gaa	ctt	gaa	agg	tac	aac	aaa	aat	tta	gaa	868
104	Phe	Gly	Gly	Gln	Lys	Lys	Glu	Leu	Glu	Arg	Tyr	Asn	Lys	Asn	Leu	Glu	
105						270			275			280					
107	gaa	gct	aaa	gga	att	ggg	ata	aag	aaa	gct	atc	acg	gcc	aac	att	tct	916
108	Glu	Ala	Lys	Gly	Ile	Gly	Ile	Lys	Lys	Ala	Ile	Thr	Ala	Asn	Ile	Ser	
109						285			290			295			300		
111	att	ggt	gcc	gct	ttc	tta	ttg	atc	tat	gca	tca	tat	gct	ctg	gct	ttc	964
112	Ile	Gly	Ala	Ala	Phe	Leu	Leu	Ile	Tyr	Ala	Ser	Tyr	Ala	Leu	Ala	Phe	
113						305			310			315					
115	tgg	tat	ggg	acc	tcc	ttg	gtc	ctc	tcc	agt	gaa	tat	tct	att	gga	caa	1012
116	Trp	Tyr	Gly	Thr	Ser	Leu	Val	Leu	Ser	Ser	Glu	Tyr	Ser	Ile	Gly	Gln	
117						320			325			330					
119	gta	ctc	act	gtc	ttc	ttt	tct	gta	tta	att	ggg	gct	ttt	agt	att	gga	1060
120	Val	Leu	Thr	Val	Phe	Phe	Ser	Val	Leu	Ile	Gly	Ala	Phe	Ser	Ile	Gly	
121						335			340			345					
123	cag	gca	tcc	cca	agc	att	gaa	gca	ttt	gca	aac	gca	aga	gga	gca	gct	1108
124	Gln	Ala	Ser	Pro	Ser	Ile	Glu	Ala	Phe	Ala	Asn	Ala	Arg	Gly	Ala	Ala	
125						350			355			360					
127	tat	gaa	atc	ttc	aag	ata	att	gac	aat	aaa	cca	agc	att	gac	agc	tat	1156
128	Tyr	Glu	Ile	Phe	Lys	Ile	Ile	Asp	Asn	Lys	Pro	Ser	Ile	Asp	Ser	Tyr	

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129	365	370	375	380	
131	tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc				1204
132	Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe				
133	385	390	395		
135	aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta				1252
136	Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu				
137	400	405	410		
139	aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt				1300
140	Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val				
141	415	420	425		
143	ggg aac agt ggc tgc ggg aag acg acc gtg cag ctg atg cag agg				1348
144	Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg				
145	430	435	440		
147	ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att				1396
148	Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile				
149	445	450	455	460	
151	agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt				1444
152	Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser				
153	465	470	475		
155	cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat				1492
156	Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr				
157	480	485	490		
159	ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa				1540
160	Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu				
161	495	500	505		
163	gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act				1588
164	Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr				
165	510	515	520		
167	ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga				1636
168	Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg				
169	525	530	535	540	
171	atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg				1684
172	Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu				
173	545	550	555		
175	gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag				1732
176	Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln				
177	560	565	570		
179	gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct				1780
180	Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala				
181	575	580	585		
183	cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat				1828
184	His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp				
185	590	595	600		
187	gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag				1876
188	Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu				
189	605	610	615	620	
191	aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa				1924
192	Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu				
193	625	630	635		

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195	att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc	1972
196	Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala	
197	640 645 650	
199	ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga	2020
200	Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg	
201	655 660 665	
203	tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt	2068
204	Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu	
205	670 675 680	
207	ggg aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg	2116
208	Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp	
209	685 690 695 700	
211	agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt	2164
212	Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly	
213	705 710 715	
215	ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata	2212
216	Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile	
217	720 725 730	
219	ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa	2260
220	Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu	
221	735 740 745	
223	aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt	2308
224	Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu	
225	750 755 760	
227	gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc	2356
228	Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly	
229	765 770 775 780	
231	aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga	2404
232	Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg	
233	785 790 795	
235	tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc	2452
236	Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr	
237	800 805 810	
239	act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa	2500
240	Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys	
241	815 820 825	
243	ggg gct ata ggt tcc agg ctt gtc att acc cag aat ata gca aat	2548
244	Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn	
245	830 835 840	
247	cgt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca	2596
248	Leu Gly Thr Gly Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr	
249	845 850 855 860	
251	ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt	2644
252	Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val	
253	865 870 875	
255	gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta	2692
256	Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu	
257	880 885 890	
259	gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act	2740

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260	Glu	Gly	Ala	Gly	Lys	Ile	Ala	Thr	Glu	Ala	Ile	Glu	Asn	Phe	Arg	Thr	
261			895				900					905					
263	gtt	gtt	tct	ttg	act	cgg	gag	cag	aag	ttt	gaa	tac	atg	tat	gca	cag	2788
264	Val	Val	Ser	Leu	Thr	Arg	Glu	Gln	Lys	Phe	Glu	Tyr	Met	Tyr	Ala	Gln	
265			910				915				920						
267	agt	ttg	caa	gtt	cca	tac	aga	aac	tct	ttg	agg	aaa	gca	cac	atc	ttc	2836
268	Ser	Leu	Gln	Val	Pro	Tyr	Arg	Asn	Ser	Leu	Arg	Lys	Ala	His	Ile	Phe	
269			925				930			935			940				
271	ggg	gtc	tca	ttt	tct	atc	acc	cag	gca	atg	atg	tat	ttt	tcc	tat	gct	2884
272	Gly	Val	Ser	Phe	Ser	Ile	Thr	Gln	Ala	Met	Met	Tyr	Phe	Ser	Tyr	Ala	
273			945				950			955							
275	ggc	tgt	ttc	cgg	ttt	ggt	gcc	tac	ttg	gtg	gca	aat	gag	ttc	atg	aac	2932
276	Gly	Cys	Phe	Arg	Phe	Gly	Ala	Tyr	Leu	Val	Ala	Asn	Glu	Phe	Met	Asn	
277			960				965			970							
279	ttt	cag	gat	gtt	ctt	ttg	gta	ttc	tca	gct	att	gtc	ttt	ggt	gcc	atg	2980
280	Phe	Gln	Asp	Val	Leu	Leu	Val	Phe	Ser	Ala	Ile	Val	Phe	Gly	Ala	Met	
281			975				980			985							
283	gca	gtg	ggg	cag	gtc	agt	tca	ttt	gct	cct	gac	tat	gcc	aaa	gcc	aaa	3028
284	Ala	Val	Gly	Gln	Val	Ser	Ser	Phe	Ala	Pro	Asp	Tyr	Ala	Lys	Ala	Lys	
285			990				995			1000							
287	gta	tca	gca	gcc	cac	gtc	atc	atc	atc	att	gaa	aaa	agc	cct	ctg	att	3076
288	Val	Ser	Ala	Ala	His	Val	Ile	Met	Ile	Ile	Glu	Lys	Ser	Pro	Leu	Ile	
289			1005				1010			1015			1020				
291	gac	agc	tac	agc	cct	cac	ggc	ctc	aag	cca	aat	acg	ttg	gaa	gga	aat	3124
292	Asp	Ser	Tyr	Ser	Pro	His	Gly	Leu	Lys	Pro	Asn	Thr	Leu	Glu	Gly	Asn	
293			1025				1030			1035							
295	gtg	aca	ttt	aat	gag	gtc	gtg	ttc	aac	tat	ccc	act	cga	cca	gac	atc	3172
296	Val	Thr	Phe	Asn	Glu	Val	Val	Phe	Asn	Tyr	Pro	Thr	Arg	Pro	Asp	Ile	
297			1040				1045			1050							
299	ccc	gtg	ctc	cag	ggg	ctg	agc	ctc	gag	gtg	aag	aag	ggc	cag	acg	ctg	3220
300	Pro	Val	Leu	Gln	Gly	Leu	Ser	Leu	Glu	Val	Lys	Lys	Gly	Gln	Thr	Leu	
301			1055				1060			1065							
303	gcc	ctc	gta	ggt	agc	agt	ggc	tgt	ggg	aag	agc	aca	gtt	gtt	cag	ctc	3268
304	Ala	Leu	Val	Gly	Ser	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Val	Val	Gln	Leu	
305			1070				1075			1080							
307	cta	gag	cgc	ttc	tat	gac	ccc	ttg	gct	ggt	tca	gtg	cta	att	gat	ggc	3316
308	Leu	Glu	Arg	Phe	Tyr	Asp	Pro	Leu	Ala	Gly	Ser	Val	Leu	Ile	Asp	Gly	
309			1085				1090			1095			1100				
311	aaa	gag	ata	aag	cac	ctg	aat	gtc	cag	tgg	ctc	cga	gca	cac	ctg	ggc	3364
312	Lys	Glu	Ile	Lys	His	Leu	Asn	Val	Gln	Trp	Leu	Arg	Ala	His	Leu	Gly	
313			1105				1110			1115							
315	atc	gtg	tct	cag	gag	ccc	atc	ctg	ttt	gac	tgc	agc	att	gcc	gag	aac	3412
316	Ile	Val	Ser	Gln	Glu	Pro	Ile	Leu	Phe	Asp	Cys	Ser	Ile	Ala	Glu	Asn	
317			1120				1125			1130							
319	att	gcc	tat	gga	gac	aac	agc	cg	gtc	gta	tca	cat	gaa	gag	att	atg	3460
320	Ile	Ala	Tyr	Gly	Asp	Asn	Ser	Arg	Val	Val	Ser	His	Glu	Glu	Ile	Met	
321			1135				1140			1145							
323	cag	gca	gcc	aag	gag	gcc	aac	ata	cac	cac	ttc	atc	gag	aca	ctc	cct	3508
324	Gln	Ala	Ala	Lys	Glu	Ala	Asn	Ile	His	His	Phe	Ile	Glu	Thr	Leu	Pro	

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Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\10222002\I672725B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; N Pos. 1,2